

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Brow, Mary Ann D.
Grotelueschen Hall, Jeff S.
Lyamichev, Victor
Olive, David M.
Prudent, James R.
- (ii) TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES BY
INVADER-DIRECTED CLEAVAGE
- (iii) NUMBER OF SEQUENCES: 69
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Medlen & Carroll
(B) STREET: 220 Montgomery Street, Suite 2200
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: United States Of America
(F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 11-JUL-1996
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/599,491
(B) FILING DATE: 24-JAN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ingolia, Diane E.
(B) REGISTRATION NUMBER: 40,027
(C) REFERENCE/DOCKET NUMBER: FORS-02306
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 705-8410
(B) TELEFAX: (415) 397-8338

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGGGGA TGCTGCCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC 60
CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG 120

GTGCAGGCGG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTCAAGGA	GGACGGGGAC	180
GCGGTGATCG	TGGTCTTTGA	CGCCAAGGCC	CCCTCCTTCC	GCCACGAGGC	CTACGGGGGG	240
TACAAGGCGG	GCCGGGCCCC	CACGCCGGAG	GACTTTCCCC	GGCAACTCGC	CCTCATCAAG	300
GAGCTGGTGG	ACCTCCTGGG	GCTGGCGCGC	CTCGAGGTCC	CGGGCTACGA	GGCGGACGAC	360
GTCCTGGCCA	GCCTGGCCAA	GAAGGCGGAA	AAGGAGGGCT	ACGAGGTCCG	CATCCTCACC	420
GCCGACAAAG	ACCTTTACCA	GCTCCTTTCC	GACCGCATCC	ACGTCCCTCA	CCCCGAGGGG	480
TACCTCATCA	CCCCGGCCTG	GCTTTGGGAA	AAGTACGGCC	TGAGGCCCCA	CCAGTGGGCC	540
GACTACCGGG	CCCTGACCGG	GGACGAGTCC	GACAACCTTC	CCGGGGTCAA	GGGCATCGGG	600
GAGAAGACGG	CGAGGAAGCT	TCTGGAGGAG	TGGGGGAGCC	TGGAAGCCCT	CCTCAAGAAC	660
CTGGACCGGC	TGAAGCCCGC	CATCCGGGAG	AAGATCCTGG	CCCACATGGA	CGATCTGAAG	720
CTCTCCTGGG	ACCTGGCCAA	GGTGCGCACC	GACCTGCCCC	TGGAGGTGGA	CTTCGCCAAA	780
AGGCGGGAGC	CCGACCGGGA	GAGGCTTAGG	GCCTTTCTGG	AGAGGCTTGA	GTTTGGCAGC	840
CTCCTCCACG	AGTTCGGCCT	TCTGGAAAGC	CCCAAGGCCC	TGGAGGAGGC	CCCCTGGCCC	900
CCGCCGGAAG	GGGCCTTCGT	GGGCTTTGTG	CTTTCCCGCA	AGGAGCCCAT	GTGGGCCGAT	960
CTTCTGGCCC	TGGCCGCCGC	CAGGGGGGGC	CGGGTCCACC	GGGCCCCCGA	GCCTTATAAA	1020
GCCCTCAGGG	ACCTGAAGGA	GGCGCGGGGG	CTTCTCGCCA	AAGACCTGAG	CGTTCCTGGCC	1080
CTGAGGGAAG	GCCTTGGCCT	CCCGCCCGGC	GACGACCCCA	TGCTCCTCGC	CTACCTCCTG	1140
GACCCTTCCA	ACACCACCCC	CGAGGGGGTG	GCCCCGCGCT	ACGGCGGGGA	GTGGACGGAG	1200
GAGGCGGGGG	AGCGGGCCGC	CCTTTCCGAG	AGGCTCTTCG	CCAACCTGTG	GGGGAGGCTT	1260
GAGGGGGAGG	AGAGGCTCCT	TTGGCTTTAC	CGGGAGGTGG	AGAGGCCCCCT	TTCCGCTGTC	1320
CTGGCCCACA	TGGAGGCCAC	GGGGGTGCGC	CTGGACGTGG	CCTATCTCAG	GGCCTTGTC	1380
CTGGAGGTGG	CCGAGGAGAT	CGCCCGCCTC	GAGGCCGAGG	TCTTCCGCCT	GGCCGGCCAC	1440
CCCTTCAACC	TCAACTCCCG	GGACCAGCTG	GAAAGGGTCC	TCTTTGACGA	GCTAGGGCTT	1500
CCCCCATCG	GCAAGACGGA	GAAGACCGGC	AAGCGCTCCA	CCAGCGCCGC	CGTCTTGGAG	1560
GCCCTCCGCG	AGGCCACCCC	CATCGTGGAG	AAGATCCTGC	AGTACCGGGA	GCTCACCAAG	1620
CTGAAGAGCA	CCTACATTGA	CCCCTTGCCG	GACCTCATCC	ACCCCAGGAC	GGGCCGCCTC	1680
CACACCCGCT	TCAACCAGAC	GGCCACGGCC	ACGGGCAGGC	TAAGTAGCTC	CGATCCCAAC	1740
CTCCAGAACA	TCCCCGTCCG	CACCCCGCTT	GGGCAGAGGA	TCCGCCGGGC	CTTCATCGCC	1800
GAGGAGGGGT	GGCTATTGGT	GGCCCTGGAC	TATAGCCAGA	TAGAGCTCAG	GGTGCTGGCC	1860
CACCTCTCCG	GCGACGAGAA	CCTGATCCGG	GTCTTCCAGG	AGGGGCGGGA	CATCCACACG	1920
GAGACCGCCA	GCTGGATGTT	CGGCGTCCCC	CGGGAGGCCG	TGGACCCCTT	GATGCGCCGG	1980

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GCGGCCAAGA	CCATCAACTT	CGGGGTCCTC	TACGGCATGT	CGGCCCACCG	CCTCTCCCAG	2040
GAGCTAGCCA	TCCCTTACGA	GGAGGCCAG	GCCTTCATTG	AGCGCTACTT	TCAGAGCTTC	2100
CCCAAGGTGC	GGGCCTGGAT	TGAGAAGACC	CTGGAGGAGG	GCAGGAGGCG	GGGGTACGTG	2160
GAGACCCTCT	TCGGCCGCCG	CCGCTACGTG	CCAGACCTAG	AGGCCCCGGGT	GAAGAGCGTG	2220
CGGGAGGCGG	CCGAGCGCAT	GGCCTTCAAC	ATGCCCCTCC	AGGGCACCGC	CGCCGACCTC	2280
ATGAAGCTGG	CTATGGTGAA	GCTCTTCCCC	AGGCTGGAGG	AAATGGGGGC	CAGGATGCTC	2340
CTTCAGGTCC	ACGACGAGCT	GGTCCTCGAG	GCCCCAAAAG	AGAGGGCGGA	GGCCGTGGCC	2400
CGGCTGGCCA	AGGAGGTCAT	GGAGGGGGTG	TATCCCCTGG	CCGTGCCCCCT	GGAGGTGGAG	2460
GTGGGGATAG	GGGAGGACTG	GCTCTCCGCC	AAGGAGTGAT	ACCACC		2506

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGATGC	TTCCCCTCTT	TGAGCCCCAA	GGCCGCGTGC	TCCTGGTGGA	CGGCCACCAC	60
CTGGCCTACC	GCACCTTCTT	TGCCCTCAAG	GGCCTCACCA	CCAGCCGCGG	CGAACCCGTT	120
CAGGCGGTCT	ACGGCTTCGC	CAAAAGCCTC	CTCAAGGCCC	TGAAGGAGGA	CGGGGACGTG	180
GTGGTGGTGG	TCTTTGACGC	CAAGGCCCCC	TCCTTCCGCC	ACGAGGCCTA	CGAGGCCTAC	240
AAGGCGGGCC	GGGCCCCCAC	CCCGGAGGAC	TTTCCCCGGC	AGCTGGCCCT	CATCAAGGAG	300
TTGGTGGACC	TCCTAGGCCT	TGTGCGGCTG	GAGGTTCCCG	GCTTTGAGGC	GGACGACGTG	360
CTGGCCACCC	TGGCCAAGCG	GGCGGAAAAG	GAGGGGTACG	AGGTGCGCAT	CCTCACTGCC	420
GACCGCGACC	TCTACCAGCT	CCTTTCGGAG	CGCATCGCCA	TCCTCCACCC	TGAGGGGTAC	480
CTGATCACCC	CGGCGTGGCT	TTACGAGAAG	TACGGCCTGC	GCCCCGAGCA	GTGGGTGGAC	540
TACCGGGCCC	TGGCGGGGGA	CCCCTCGGAT	AACATCCCCG	GGGTGAAGGG	CATCGGGGAG	600
AAGACCGCCC	AGAGGCTCAT	CCGCGAGTGG	GGGAGCCTGG	AAAACCTCTT	CCAGCACCTG	660
GACCAGGTGA	AGCCCTCCTT	GCGGGAGAAG	CTCCAGGCGG	GCATGGAGGC	CCTGGCCCTT	720
TCCCGGAAGC	TTTCCCAGGT	GCACACTGAC	CTGCCCCTGG	AGGTGGACTT	CGGGAGGCGC	780
CGCACACCCA	ACCTGGAGGG	TCTGCGGGCT	TTTTTTGGAGC	GGTTGGAGTT	TGGAAGCCTC	840
CTCCACGAGT	TCGGCCTCCT	GGAGGGGCCG	AAGGCGGCAG	AGGAGGCCCC	CTGGCCCCCT	900
CCGGAAGGGG	CTTTTTTGGG	CTTTTCCTTT	TCCCGTCCCG	AGCCCATGTG	GGCCGAGCTT	960

CTGGCCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGGC	1020
CTGAGGGACC TTAAGGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG	1080
CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC	1140
CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT	1200
GCGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG	1260
GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGGTGTTG	1320
GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG	1380
GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC	1440
TTCAACCTCA ACTCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT	1500
GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC	1560
CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC	1620
AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC	1680
ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCACCTG	1740
CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG	1800
GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCAC	1860
CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG	1920
ACCGCCAGCT GGATGTTTCG CGTTTCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG	1980
GCCAAGACCA TCAACTTCG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG	2040
CTTTCCATCC CCTACGAGGA GGCAGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC	2100
AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG	2160
ACCCTCTTCG GCCGCCGGCG CTATGTGCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC	2220
GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG	2280
AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG	2340
CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCAAGGACC GGGCGGAGAG GGTAGCCGCT	2400
TTGGCCAAGG AGGTCATGGA GGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG	2460
GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG	2496

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

1007439 02420 302120

ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC	180
AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC	360
GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC	420
ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG	480
GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG	540
GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG	660
AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC	720
CTCAGGCTCT CCTTGGAGCT CTCCCAGGGT CGCACCGACC TCCCCCTGGA GGTGGACCTC	780
GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC	840
GGCAGCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC	900
TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCCTCT CCCGCCCCGA GCCCATGTGG	960
GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC	1020
TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC	1080
TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCCATGCT CCTCGCCTAC	1140
CTCCTGGACC CCTCCAACAC CACCCCCGAG GGGGTGGCGC GGCGCTACGG GGGGGAGTGG	1200
ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG	1260
CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCTCTCC	1320
CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC	1380
CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG	1440
GGCCACCCCT TCAACCTCAA CTCCCAGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT	1500
AGGCTTCCCG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG	1560
CTGGAGGCCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC	1620
ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC	1680
CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC	1740
CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC	1800

GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC 1860
 CTCGCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC 1920
 CACACCCAGA CCGCAAGCTG GATGTTTCGGC GTCCCCCGG AGGCCGTGGA CCCCCTGATG 1980
 CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040
 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100
 GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT 2160
 ACGTGGAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220
 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG 2280
 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCGCCT CCGGGAGATG GGGGCCCGCA 2340
 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG 2400
 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG 2460
 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG 2504

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
 1 5 10 15
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
 20 25 30
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
 50 55 60
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
 65 70 75 80
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
 85 90 95
 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
 100 105 110
 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
 115 120 125
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
 130 135 140

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Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	145	150	155	160
Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	165	170	175	
Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	180	185	190	
Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	195	200	205	
Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	210	215	220	
Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	225	230	235	240
Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	245	250	255	
Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	Phe	260	265	270	
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	275	280	285	
Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	290	295	300	
Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp	305	310	315	320
Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro	325	330	335	
Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu	340	345	350	
Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	Pro	355	360	365	
Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	370	375	380	
Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	385	390	395	400
Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	Leu	405	410	415	
Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu	420	425	430	
Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	435	440	445	
Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala	450	455	460	
Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	465	470	475	480

2025-03-27

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
820 825 830

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15
 Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30
 Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45
 Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val
50 55 60
 Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr
65 70 75 80
 Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95
 Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val
100 105 110
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala
115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140
 Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr
145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu
165 170 175
 Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg
195 200 205
 Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys
210 215 220
 Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu
225 230 235 240
 Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp
245 250 255

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Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Val	Leu	Val	Val	Leu
	595						600					605			
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp
	610					615					620				
Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Gln
	625				630					635					640
Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Ser	Pro	Glu	Gly	Val	Asp	Pro	Leu
				645					650					655	
Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met
			660					665					670		
Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ser	Ile	Pro	Tyr	Glu	Glu	Ala
		675					680					685			
Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	Ala
	690					695					700				
Trp	Ile	Glu	Gly	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu
	705				710					715					720
Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val
				725					730					735	
Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val
			740					745					750		
Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Arg	Leu	Phe
		755					760					765			
Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp
	770					775					780				
Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Asp	Arg	Ala	Glu	Arg	Val	Ala	Ala
	785				790					795					800
Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Trp	Pro	Leu	Gln	Val	Pro	Leu
				805					810					815	
Glu	Val	Glu	Val	Gly	Leu	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	
			820					825					830		

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
			20					25					30		

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Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	35	40	45
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	Val	Phe	50	55	60
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	65	70	75
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	115	120	125
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	130	135	140
Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu	145	150	155
Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175
Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp	180	185	190
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu	195	200	205
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220
Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	Glu	Asp	225	230	235
Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	245	250	255
Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg	260	265	270
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	275	280	285
Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	290	295	300
Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	305	310	315
Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Asp	Gly	Arg	Val	His	Arg	325	330	335
Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	340	345	350
Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	355	360	365

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Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	370	375	380
Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	385	390	395
Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	405	410	415
Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	420	425	430
His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	435	440	445
Thr	Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	450	455	460
Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	465	470	475
Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	485	490	495
Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys	Thr	Gly	500	505	510
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	515	520	525
Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	530	535	540
Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	545	550	555
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	565	570	575
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	580	585	590
Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	595	600	605
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	610	615	620
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	625	630	635
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	645	650	655
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	660	665	670
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	675	680	685
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	690	695	700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
725 730 735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
770 775 780

Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
820 825 830

Lys Gly

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2502 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGNNGGCGA TGCTTCCCCT CTTTGAGCCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CTTGCGCCCTG AAGGGCCTCA CCACCAGCCG GGGCGAACC	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGGAC	180
NNGGCGGTGN TCGTGGTCTT TGACGCCAAG GCCCCTCCT TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG CGGGCCGGGC CCCCACCCCG GAGGACTTTC CCCGGCAGCT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTTGCG CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC	360
GACGTNCTGG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC	420
ACCGCCGACC GCGACCTCTA CCAGCTCCTT TCCGACCGCA TCGCCGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC GTGGCTTTGG GAGAAGTACG GCCTGAGGCC GGAGCAGTGG	540
GTGGACTACC GGGCCCTGGC GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CCGCCCNAA GCTCCTCNAG GAGTGGGGGA GCCTGGAAAA CCTCCTCAAG	660
AACCTGGACC GGGTGAAGCC CGCCNTCCGG GAGAAGATCC AGGCCACAT GGANGACCTG	720

ANGCTCTCCT	GGGAGCTNTC	CCAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAGNGGCGGG	AGCCCGACCG	GGAGGGGCTT	AGGGCCTTTC	TGGAGAGGCT	GGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTCCTGGAG	GGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTTT	GTCTTTTCCC	GCCCCGAGCC	CATGTGGGCC	960
GAGCTTCTGG	CCCTGGCCGC	CGCCAGGGAG	GGCCGGGTCC	ACCGGGCACC	AGACCCCTTT	1020
ANGGGCCTNA	GGGACCTNAA	GGAGGTGCGG	GGNCTCCTCG	CCAAGGACCT	GGCCGTTTTG	1080
GCCCTGAGGG	AGGGCCTNGA	CCTCNTGCCC	GGGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCCT	CCAACACCAC	CCCCGAGGGG	GTGGCCCCGGC	GCTACGGGGG	GGAGTGGACG	1200
GAGGANGCGG	GGGAGCGGGC	CCTCCTNTCC	GAGAGGCTCT	TCCNGAACCT	NNNGCAGCGC	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCAGGAGG	TGGAGAAGCC	CCTTTCCCGG	1320
GTCTTGCCCC	ACATGGAGGC	CACGGGGGTN	CGGCTGGACG	TGGCCTACCT	CCAGGCCCTN	1380
TCCCTGGAGG	TGGCGGAGGA	GATCCGCCGC	CTCGAGGAGG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TGCTCTTTGA	CGAGCTNGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACN	GGCAAGCGCT	CCACCAGCGC	CGCCGTGCTG	1560
GAGGCCCTNC	GNGAGGCCCA	CCCCATCGTG	GAGAAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTCAAGA	ACACCTACAT	NGACCCCTG	CCNGNCCTCG	TCCACCCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTTAGTAG	CTCCGACCCC	1740
AACCTGCAGA	ACATCCCCGT	CCGCACCCCN	CTGGGCCAGA	GGATCCGCCG	GGCCTTCGTG	1800
GCCGAGGAGG	GNTGGGTGTT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CCGGGTCCTG	1860
GGCCACCTCT	CCGGGGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGAG	GGACATCCAC	1920
ACCCAGACCG	CCAGCTGGAT	GTTCGGCGTC	CCCCCGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCCGCCCA	CCGCCTCTCC	2040
CAGGAGCTTG	CCATCCCCTA	CGAGGAGGCG	GTGGCCTTCA	TTGAGCGCTA	CTTCCAGAGC	2100
TTCCCAAGG	TGCGGGCCTG	GATTGAGAAG	ACCCTGGAGG	AGGGCAGGAG	GCGGGGGTAC	2160
GTGGAGACCC	TCTTCGGCCG	CCGGCGCTAC	GTGCCCCGACC	TCAACGCCCC	GGTGAAGAGC	2220
GTGCGGGAGG	CGGCGGAGCG	CATGGCCTTC	AACATGCCCG	TCCAGGGCAC	CGCCGCCGAC	2280
CTCATGAAGC	TGGCCATGGT	GAAGCTCTTC	CCCCGGCTNC	AGGAAATGGG	GGCCAGGATG	2340
CTCCTNCAGG	TCCACGACGA	GCTGGTCCTC	GAGGCCCCCA	AAGAGCGGGC	GGAGGNGGTG	2400
GCCGCTTTGG	CCAAGGAGGT	CATGGAGGGG	GTCTATCCCC	TGGCCGTGCC	CCTGGAGGTG	2460
GAGGTGGGGA	TGGGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	AG		2502

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 833 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Xaa	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	1	5	10	15
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	20	25	30	
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	35	40	45	
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Xaa	Val	50	55	60	
Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	Ala	65	70	75	80
Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	85	90	95	
Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Xaa	Arg	Leu	Glu	100	105	110	
Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	115	120	125	
Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	130	135	140	
Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	Ala	Val	Leu	His	Pro	Glu	Gly	145	150	155	160
Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	165	170	175	
Glu	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Xaa	Gly	Asp	Pro	Ser	Asp	Asn	180	185	190	
Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Xaa	Lys	Leu	Leu	195	200	205	
Xaa	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Val	210	215	220	
Lys	Pro	Xaa	Xaa	Arg	Glu	Lys	Ile	Xaa	Ala	His	Met	Glu	Asp	Leu	Xaa	225	230	235	240
Leu	Ser	Xaa	Xaa	Leu	Ser	Xaa	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	245	250	255	
Asp	Phe	Ala	Xaa	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg	Ala	Phe	260	265	270	

Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu
		275					280					285			
Glu	Xaa	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly
	290					295					300				
Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu
305					310					315					320
Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Xaa	Gly	Arg	Val	His	Arg	Ala	Xaa
				325					330					335	
Asp	Pro	Leu	Xaa	Gly	Leu	Arg	Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu	Leu
			340					345					350		
Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Asp	Leu	Xaa
		355					360					365			
Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn
	370					375					380				
Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu
385					390					395					400
Asp	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Phe	Xaa	Asn	Leu
				405					410					415	
Xaa	Xaa	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Xaa	Glu
			420					425					430		
Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly
		435					440					445			
Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	Ala
	450					455					460				
Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	His
465					470					475					480
Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp
				485					490					495	
Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg
			500					505					510		
Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile
		515					520					525			
Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	Thr
	530					535					540				
Tyr	Ile	Asp	Pro	Leu	Pro	Xaa	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	Leu
545					550					555					560
His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser
				565					570					575	
Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln
			580					585					590		
Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Xaa	Leu	Val	Ala
		595					600					605			

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Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
660 665 670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
690 695 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
725 730 735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala
785 790 795 800

Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
805 810 815

Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu
820 825 830

Xaa

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180

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GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTTCG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGCGG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCCGCT	1320
GTCCTGGCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGGCATG	CAAGCTTGGC	1620
ACTGGCCGTC	GTTTTACAAC	GTCGTGA				1647

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2088 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION:. SEQ ID NO:10:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC 60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG 120
CCGGTGCAGG CGGTCTACGG CTTGCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG 180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG 240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC 300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC 360
GACGTCCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC 420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG 480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCACTGG 540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC 600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG 660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG 720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC 780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC 840
AGCCTCCTCC ACGAGTTCGG CTTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG 900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC 960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT 1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG 1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GCGGACGACC CCATGCTCCT CGCCTACCTC 1140
CTGGACCCTT CCAACACCAC CCCCAGGGGG GTGGCCCCGGC GCTACGGCGG GGAGTGGACG 1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG 1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCCGCT 1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG 1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC 1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAGGG TCCTCTTTGA CGAGCTAGGG 1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG 1560
GAGGCCCTCC GCGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC 1620
AAGCTGAAGA GCACCTACAT TGACCCCTTG CCGGACCTCA TCCACCCAG GACGGGCCGC 1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGGCA GGCTAAGTAG CTCCGATCCC 1740
AACCTCCAGA ACATCCCCGT CCGCACCCCG CTTGGGCAGA GGATCCGCGG GGCCTTCATC 1800

GCCGAGGAGG GGTGGCTATT GGTGGCCCTG GACTATAGCC AGATAGAGCT CAGGGTGCTG	1860
GCCCCACCTCT CCGGCGACGA GAACCTGATC CGGGTCTTCC AGGAGGGGCG GGACATCCAC	1920
ACGGAGACCG CCAGCTGGAT GTTCGGCGTC CCCCgggAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCGGCCCA CCGCCTCTCC	2040
CAGGAGCTAG CTAGCCATCC CTTACGAGGA GGCCCAGGCC TTCATTGA	2088

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 962 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCAAGGGCC GGTCTCCTCT GGTGGACGGC	60
CACCACCTGG CCTACGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG	120
CCGGTGCAGG CCGTCTACGG CTTGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCTTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTTCTT TCCGACCGCA TCCACGTCCT CCACCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC	840
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGT CATGGAGGGG GTGTATCCCC	900
TGGCCGTGCC CCTGGAGGTG GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT	960
GA	962

10074328.021202

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAATTCG GGGATGCTGC CCCTCTTTGA GCCCAAGGGC CGGGTCCTCC TGGTGGACGG 60
CCACCACCTG GCCTACCGCA CCTTCCACGC CTTGAAGGGC CTCACCACCA GCCGGGGGGA 120
GCCGGTGCAG GCGGTCTACG GCTTCGCCAA GAGCCTCCTC AAGGCCCTCA AGGAGGACGG 180
GGACGCGGTG ATCGTGGTCT TTGACGCCAA GGCCCCCTCC TTCCGCCACG AGGCCTACGG 240
GGGGTACAAG GCGGGCCGGG CCCCCACGCC GGAGGACTTT CCCC GGCAAC TCGCCCTCAT 300
CAAGGAGCTG GTGGACCTCC TGGGGCTGGC GCGCCTCGAG GTCCCGGGCT ACGAGGCGGA 360
CGACGTCCTG GCCAGCCTGG CCAAGAAGGC GGAAAAGGAG GGCTACGAGG TCCGCATCCT 420
CACCGCCGAC AAAGACCTTT ACCAGCTCCT TTCCGACCGC ATCCACGTCC TCCACCCCGA 480
GGGGTACCTC ATCACCCCGG CCTGGCTTTG GGAAAAGTAC GGCCTGAGGC CCGACCAGTG 540
GGCCGACTAC CGGGCCCTGA CCGGGGACGA GTCCGACAAC CTTCCCGGGG TCAAGGGCAT 600
CGGGGAGAAG ACGGCGAGGA AGCTTCTGGA GGAGTGGGGG AGCCTGGAAG CCCTCCTCAA 660
GAACCTGGAC CGGCTGAAGC CCGCCATCCG GGAGAAGATC CTGGCCCACA TGGACGATCT 720
GAAGCTCTCC TGGGACCTGG CCAAGGTGCG CACCGACCTG CCCCTGGAGG TGGACTTTCG 780
CAAAAGGCGG GAGCCCGACC GGGAGAGGCT TAGGGCCTTT CTGGAGAGGC TTGAGTTTGG 840
CAGCCTCCTC CACGAGTTCG GCCTTCTGGA AAGCCCCAAG ATCCGCCGGG CCTTCATCGC 900
CGAGGAGGGG TGGCTATTGG TGGCCCTGGA CTATAGCCAG ATAGAGCTCA GGGTGCTGGC 960
CCACCTCTCC GGCGACGAGA ACCTGATCCG GGTCTTCCAG GAGGGGCGGG ACATCCACAC 1020
GGAGACCGCC AGCTGGATGT TCGGCGTCCC CCGGGAGGCC GTGGACCCCC TGATGCGCCG 1080
GGCGGCCAAG ACCATCAACT TCGGGGTCCT CTACGGCATG TCGGCCCACC GCCTCTCCCA 1140
GGAGCTAGCC ATCCCTTACG AGGAGGCCCA GGCTTTCATT GAGCGCTACT TTCAGAGCTT 1200
CCCCAAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC GGGGGTACGT 1260
GGAGACCCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA GAGGCCCAGG TGAAGAGCGT 1320
GCGGGAGGCG GCCGAGCGCA TGGCCTTCAA CATGCCCCGTC CGGGGCACCG CCGCCGACCT 1380
CATGAAGCTG GCTATGGTGA AGCTCTTCCC CAGGCTGGAG GAAATGGGGG CCAGGATGCT 1440
CCTTCAGGTC CACGACGAGC TGGTCCTCGA GGCCCCAAAA GAGAGGGCGG AGGCCGTGGC 1500

CCGGCTGGCC AAGGAGGTCA TGGAGGGGGT GTATCCCCTG GCCGTGCCCC TGGAGGTGGA 1560
GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA 1600

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGAATTCG GGGATGCTGC CCCTCTTTGA GCCCAA 36

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC 34

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CCGGGCGAGC TCGAATTCCG 60

TGTATTCTAT AGTGTCACCT AAATCGAATT C 91

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATACGACT CACTATAGGG 20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGATT TAGGTGACAC TATAGAA

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG

42

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC

30

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

10074328 021203

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCTCTG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCACTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTIONGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGCC	840
AGCCTCCTCC ACGAGTTCCG CTTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG	1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GCGGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCTT CCAACACCAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TCCTCTTTGA CGAGCTAGGG	1500

10074320 021202

CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG 1560
GAGGCCCTCC GCGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC 1620
AAGCTGAAGA GCACCTACAT TGACCCCTTG CCGGACCTCA TCCACCCAG GACGGGCCGC 1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGGCA GGCTAAGTAG CTCCGATCCC 1740
AACCTCCAGA ACATCCCCGT CCGCACCCCG CTTGGGCAGA GGATCCGCCG GGCCTTCATC 1800
GCCGAGGAGG GGTGGCTATT GGTGGCCCTG GACTATAGCC AGATAGAGCT CAGGGTGCTG 1860
GCCCACCTCT CCGGCGACGA GAACCTGATC CGGGTCTTCC AGGAGGGGCG GGACATCCAC 1920
ACGGAGACCG CCAGCTGGAT GTTCGGCGTC CCCCGGGAGG CCGTGGACCC CCTGATGCGC 1980
CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCGGCCCA CCGCCTCTCC 2040
CAGGAGCTAG CCATCCCTTA CGAGGAGGCC CAGGCCTTCA TTGAGCGCTA CTTTCAGAGC 2100
TTCCCCAAGG TGCGGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC 2160
GTGGAGACCC TCTTCGGCCG CCGCCGCTAC GTGCCAGACC TAGAGGCCCG GGTGAAGAGC 2220
GTGCGGGAGG CGGCCGAGCG CATGGCCTTC AACATGCCCG TCCGGGGCAC CGCCGCCGAC 2280
CTCATGAAGC TGGCTATGGT GAAGCTCTTC CCCAGGCTGG AGGAAATGGG GGCCAGGATG 2340
CTCCTTCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCAA AAGAGAGGGC GGAGGCCGTG 2400
GCCCGGCTGG CCAAGGAGGT CATGGAGGGG GTGTATCCCC TGGCCGTGCC CCTGGAGGTG 2460
GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT GA 2502

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTTAGGTG AACTATAG

19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA 60
CACAGCAGAA AC 72

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTTCTGCTG TGTCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG 60
CTTGTTTCGTC 70

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG 20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTCGTCTCT CTTG 24

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGATAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC

46

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC

50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCCTC 60

TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC 120

CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC 180

GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC 240

GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC 300

ACGCCGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGG CCTCCTGGGG 360

CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG 420

AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG 480

CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG 540

CTTTGGGAAA AGTACGGCCT GAGGCCCCGAC CAGTGGGCGG ACTACCGGGC CCTGACCGGG 600
GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT 660
CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC 720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG 780
GTGCGCACCG ACCTGCCCCCT GGAGGTGGAC TTCGCCAAAA GCGGGGAGCC CGACCGGGAG 840
AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT 900
CTGGAAAGCC CCAAGTCATG GAGGGGGTGT ATCCCCTGGC CGTGCCCTG GAGGTGGAGG 960
TGGGGATAG 969

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCCTC 60
TTTGAAGCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC 120
CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC 180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC 240
GCCAAGGCC CCTCCTTCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC 300
ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGG CCTCCTGGGG 360
CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG 420
AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACC GCGACAAAGA CCTTTACCAG 480
CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG 540
CTTTGGGAAA AGTACGGCCT GAGGCCCCGAC CAGTGGGCGG ACTACCGGGC CCTGACCGGG 600
GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT 660
CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC 720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG 780
GTGCGCACCG ACCTGCCCCCT GGAGGTGGAC TTCGCCAAAA GCGGGGAGCC CGACCGGGAG 840
AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT 900
CTGGAAAGCC CCAAGGCCGC ACTCGAGCAC CACCACCACC ACCACTGA 948

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT 60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT 120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG 180
TTTCCTGTGT GAAATTGTTA TCCGCT 206

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTC TCTGCTCTCT GGTCGCTGTC TCGCTTGTTT GTC 43

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGC TTGTTGTC 19

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GACGAACAAG CGAGACAGCG 20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCTGGGTTC TCTGCTCTCT GGTC

24

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA

43

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCAGAGAGC AGAGAACCCA GAA

23

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGCTATG ACCATGATTA C

21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTTCTCTGCT CTCTGGTCGC TGTCTCGCTT GTGAAACAAG CGAGACAGCG TGGTCTCTCG 60

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGAGAGACCA CGCTG 15

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCTTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GCTTCCCCCG TC 52

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGAAAGGAAG GGAAGAAAGC GAAAGG 26

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(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GACGGGGAAA GCCGGCGAAC G

21

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAAAGCCGGC GAACGTGGCG

20

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGCGAACGTG GCGAGAAAGG A

21

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCTTTGCTT TCTTCCCTT CTTTCTCGCC ACGTTCGCCG GC

42

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(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CCTTTCGCTC TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GC

42

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 8
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/mod_base= OTHER

/note= "The A residue at this position is 2'-O-methyladenosine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGAAAGGAAG GGAAGAAAGC GAAAGGT

27

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCGGCGAAC GTGGCGAGAA AGGA

24

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTTTTCTT TGAGGTTTAG

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCGACACTCC ACCATAGAT

19

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTGTCTTCAC GCAGAAAGC

19

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCACGGTCTA CGAGACCTC

19

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGAAAGCUU GCAUGCCUGC AGGUCGACUC UAGAGGAUCU ACUAGUCAUA UGGAUUCUGU 60
CUUCACGCAG AAAGCGUCUG GCCAUGGCGU UAGUAUGAGU GUCGUGCAGC CUCCAGGACC 120
CCCCUCCCG GGAGAGGCAU AGUGGUCUGC GGAACCGGUG AGUACACCGG AAUUGCCAGG 180
ACGACCGGGU CCUUUCUUGG AUAAACCCGC UCAAUGCCUG GAGAUUUGGG CGUGCCCCCG 240
CAAGACUGCU AGCCGAGUAG UGUUGGGUCG CGAAAGGCCU UGUGGUACUG CCUGAUAGGG 300
UGCCUGCGAG UGCCCCGGA GGUCUCGUAG ACCGUGC 337

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 18
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
- /note= "The N at this position indicates the presence of a fluorescein dye on an abasic linker."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGTCGTCC TGGCAATNCC 20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GTTTATCCAA GAAAGGACCC GGTCC 25

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CAGGGTGAAG GGAAGAAGAA AGCGAAAGGT

30

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CAGGGGGAAG GGAAGAAGAA AGCGAAAGGT

30

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: modified_base
(B) LOCATION: 1..2
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/mod_base= OTHER

/note= "The T residues at positions 1 and 2 are amino modified T residues."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TTCTTTTCAC CAGCGAGACG GG

22

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATTGGGCGCC AGGGTGGTTT TT

22

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCCGTCTCGC TGGTGAAAAG AAAAACCACC CTGGCGCCCA ATACGCAAAC CGC

53

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GAATTCGATT TAGGTGACAC TATAGAATAC A

31

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CCTTTGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GC

42

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCCGGCGAAC GTGGCGAGAA AGGA

24

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202120 825400T

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CAGAAGGAAG GGAAGAAAGC GAAAGG

26

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CAGGGGGAAG GGAAGAAAGC GAAAGG

26

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGGGTACAG GGAAGAAAGC GAAAGG

26

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